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RAW SEQUENCE LISTING   DATE: 03/15/2002
PATENT APPLICATION: **US/09/612,809**   TIME: 14:31:44

Input Set : **A:\Iowa042.app**
Output Set: **N:\CRF3\03152002\I612809.raw**

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 3  <110> APPLICANT: SHEFFIELD et al., VAL C.
 5  <120> TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR CONGENITAL HEART
 6        DISEASE BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
 8  <130> FILE REFERENCE: IOWA:042USD1
10  <140> CURRENT APPLICATION NUMBER: 09/612,809
11  <141> CURRENT FILING DATE: 2000-07-10
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15  <170> SOFTWARE: PatentIn Ver. 2.1
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31  agtgtggcga gaagggcgcc tgcttgttct ttctttttgt ctgctttccc ccgtttgcgc 180
33  ctggaagctg cgccgcgagt tcctgcaagg cggtctgccg cggccgggcc cggccttctc 240
35  ccctcgcagc gaccccgcct cgcggccgcg cgggccccga ggtagcccga ggcgccggag 300
37  gagccagccc cagcgagcgc cgggagaggc ggcagcgcag ccggacgcac agcgcagcgg 360
39  gccggcacca gctcggccgg gcccggactc ggactcggcg gccggcgcgg cgcggcccgg 420
41  cccgagcgag ggtggggggc ggcgggcggc gcggggcggc ggcgagcggg ggcc atg     477
42                                                              Met
43                                                               1
45  cag gcg cgc tac tcc gtg tcc agc ccc aac tcc ctg gga gtg gtg ccc    525
46  Gln Ala Arg Tyr Ser Val Ser Ser Pro Asn Ser Leu Gly Val Val Pro
47              5               10              15
49  tac ctc ggc ggc gag cag agc tac tac cgc gcg gcg gcc gcg gcg gcc    573
50  Tyr Leu Gly Gly Glu Gln Ser Tyr Tyr Arg Ala Ala Ala Ala Ala Ala
51          20              25              30
53  ggg ggc ggc tac acc gcc atg ccg gcc ccc atg agc gtg tac tcg cac    621
54  Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser His
55          35              40              45
57  cct gcg cac gcc gag cag tac ccg ggc ggc atg gcc cgc gcc tac ggg    669
58  Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr Gly
59   50              55              60              65
61  ccc tac acg ccg cag ccg cag ccc aag gac atg gtg aag ccg ccc tat    717
62  Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro Tyr
63              70              75              80
65  agc tac atc gcg ctc atc acc atg gcc atc cag aac gcc ccg gac aag    765
66  Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp Lys
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69 aag atc acc ctg aac ggc atc tac cag ttc atc atg gac cgc ttc ccc   813
70 Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro
71         100               105               110
73 ttc tac cgg gac aac aag cag ggc tgg cag aac agc atc cgc cac aac   861
74 Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn
75     115               120               125
77 ctc tcg ctc aac gag tgc ttc gtc aag gtg ccg cgc gac gac aag aag   909
78 Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys
79 130               135               140               145
81 ccg ggc aag ggc agc tac tgg acg ctg gac ccg gac tcc tac aac atg   957
82 Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met
83             150               155               160
85 ttc gag aac ggc agc ttc ctg cgg cgg cgg cgg cgc ttc aag aag aag   1005
86 Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys Lys
87             165               170               175
89 gac gcg gtg aag gac aag gag gag aag gac agg ctg cac ctc aag gag   1053
90 Asp Ala Val Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys Glu
91         180               185               190
93 ccg ccc ccg ccc ggc cgc cag ccc ccg ccc gcg ccg ccg gag cag gcc   1101
94 Pro Pro Pro Pro Gly Arg Gln Pro Pro Pro Ala Pro Pro Glu Gln Ala
95     195               200               205
97 gac ggc aac gcg ccc ggt ccg cag ccg ccg ccc gtg cgc atc cag gac   1149
98 Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln Asp
99 210               215               220               225
101 atc aag acc gag aac ggt acg tgc ccc tcg ccg ccc cag ccc ctg tcc   1197
102 Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu Ser
103             230               235               240
105 ccg gcc gcc gcc ctg ggc agc ggc agc gcc gcc gcg gtg ccc aag atc   1245
106 Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys Ile
107         245               250               255
109 gag agc ccc gac agc agc agc agc agc ctg tcc agc ggg agc agc ccc   1293
110 Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser Pro
111         260               265               270
113 ccg ggc agc ctg ccg tcg gcg cgg ccg ctc agc ctg gac ggt gcg gat   1341
114 Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala Asp
115     275               280               285
117 tcc gcg ccg ccg ccg ccc gcg ccc tcc gcc ccg ccg ccg cac cat agc   1389
118 Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His Ser
119 290               295               300               305
121 cag ggc ttc agc gtg gac aac atc atg acg tcg ctg cgg ggg tcg ccg   1437
122 Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser Pro
123             310               315               320
125 cag agc gcg gcc gcg gag ctc agc tcc ggc ctt ctg gcc tcg gcg gcc   1485
126 Gln Ser Ala Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala Ala
127         325               330               335
129 gcg tcc tcg cgc gcg ggg atc gca ccc ccg ctg gcg ctc ggc gcc tac   1533
130 Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala Tyr
131         340               345               350
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133 tcg ccc ggc cag agc tcc ctc tac agc tcc ccc tgc agc cag acc tcc   1581
134 Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr Ser
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137 agc gcg ggc agc tcg ggc ggc ggc ggc ggc ggc gcg ggg gcc gcg ggg   1629
138 Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala Gly
139 370             375             380             385
141 ggc gcg ggc ggc gcc ggg acc tac cac tgc aac ctg caa gcc atg agc   1677
142 Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met Ser
143             390             395             400
145 ctg tac gcg gcc ggc gag cgc ggg ggc cac ttg cag ggc gcg ccc ggg   1725
146 Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro Gly
147             405             410             415
149 ggc gcg ggc ggc tcg gcc gtg gac aac ccc ctg ccc gac tac tct ctg   1773
150 Gly Ala Gly Gly Ser Ala Val Asp Asn Pro Leu Pro Asp Tyr Ser Leu
151         420             425             430
153 cct ccg gtc acc agc agc agc tcg tcg tcc ctg agt cac ggc ggc ggc   1821
154 Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly Gly
155     435             440             445
157 ggc ggc ggc ggc ggg gga ggc cag gag gcc ggc cac cac cct gcg gcc   1869
158 Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala Ala
159 450             455             460             465
161 cac caa ggc cgc ctc acc tcg tgg tac ctg aac cag gcg ggc gga gac   1917
162 His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly Asp
163             470             475             480
165 ctg ggc cac ttg gca agc gcg gcg gcg gcg gcg gcg gcc gca ggc tac   1965
166 Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly Tyr
167             485             490             495
169 ccg ggc cag cag cag aac ttc cac tcg gtg cgg gag atg ttc gag tca   2013
170 Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu Ser
171         500             505             510
173 cag agg atc ggc ttg aac aac tct cca gtg aac ggg aat agt agc tgt   2061
174 Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser Cys
175     515             520             525
177 caa atg gcc ttc cct tcc agc cag tct ctg tac cgc acg tcc gga gct   2109
178 Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly Ala
179 530             535             540             545
181 ttc gtc tac gac tgt agc aag ttt tga cacaccctca aagccgaact   2156
182 Phe Val Tyr Asp Cys Ser Lys Phe
183             550
185 aaatcgaacc ccaaagcagg aaaagctaaa ggaacccatc aaggcaaaat cgaaactaaa 2216
187 aaaaaaaaat ccaattaaaa aaaacccctg agaatattca ccacaccagc gaacagaata 2276
189 tccctccaaa aattcagctc accagcacca gcacgaagaa aactctattt tcttaaccga 2336
191 ttaattcaga gccacctcca ctttgccttg tctaaataaa caaacccgta aactgtttta 2396
193 tacagagaca gcaaaatctt ggtttattaa aggacagtgt tactccagat aacacgtaag 2456
195 tttcttcttg cttttcagag acctgctttc ccctcctccc gtctcccctc tcttgccttc 2516
197 ttccttgcct ctcacctgta agatattatt ttatcctatg ttgaagggag ggggaaagtc 2576
199 cccgtttatg aaagtcgctt tcttttttatt catggacttg ttttaaaatg taaattgcaa 2636
201 catagtaatt tattttttaat ttgtagttgg atgtcgtgga ccaaacgcca gaaagtgttc 2696
203 ccaaaacctg acgttaaatt gcctgaaact ttaaattgtg cttttttttct cattataaaa 2756
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207 tgtttgttta ttaataaatt accattcagt ttgaatgaga cctatatgtc tggatacttt 2876
209 aatagagctt taattattac gaaaaaagat ttcagagata aaacactaga agttacctat 2936
211 tctccaccta aatctctgaa aaatggagaa accctctgac tagtccatgt caaattttac 2996
213 taaaagtctt tttgtttaga tttattttcc tgcagcatct tctgcaaaat gtactatata 3056
215 gtcagcttgc tttgaggcta gtaaaaagat attttttctaa acagattgga gttggcatat 3116
217 aaacaaatac gttttctcac taatgacagt ccatgattcg gaaattttaa gcccatgaat 3176
219 cagccgcggt cttaccacgg tgatgcctgt gtgccgagag atgggactgt gcggccagat 3236
221 atgcacagat aaatatttgg cttgtgtatt ccatataaaa ttgcagtgca tattatacat 3296
223 ccctgtgagc cagatgctga atagattttt tcctattatt tcagtccttt ataaaaggaa 3356
225 aaataaacca gtttttaaat gtatgtatat aattctcccc catttacaat ccttcatgta 3416
227 ttacatagaa ggattgcttt tttaaaaata tactgcgggt tggaaaggga tatttaatct 3476
229 ttgagaaact attttagaaa atatgtttgt agaacaatta ttttttgaaaa agatttaaag 3536
231 caataacaag aaggaaggcg agaggagcag aacattttgg tctagggtgg tttctttttta 3596
233 aaccattttt tcttgttaat ttacagttaa acctagggga caatccggat tggccctccc 3656
235 ccttttgtaa ataacccagg aaatgtaata aattcattat cttagggtga tctgccctgc 3716
237 caatcagact ttggggagat ggcgatttga ttacagacgt tcggggggt ggggggcttg 3776
239 cagtttgttt tggagataat acagtttcct gctatctgcc gctcctatct agaggcaaca 3836
241 cttaagcagt aattgctgtt gcttgttgtc aaaatttgat cattgttaaa ggattgctgc 3896
243 aaataaatac actttaattt cagtcaaaaa aaaaaaaaaa aaaaaaaaa      3946
246 <210> SEQ ID NO: 2
247 <211> LENGTH: 553
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 2
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256 Ala Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser
257           35                  40                  45
258 His Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr
259       50                  55                  60
260 Gly Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro
261  65                  70                  75                  80
262 Tyr Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp
263                  85                  90                  95
264 Lys Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe
265              100                 105                 110
266 Pro Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His
267              115                 120                 125
268 Asn Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys
269      130                 135                 140
270 Lys Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn
271 145                 150                 155                 160
272 Met Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys
273                  165                 170                 175
274 Lys Asp Ala Val Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys
275              180                 185                 190
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276 Glu Pro Pro Pro Pro Gly Arg Gln Pro Pro Pro Ala Pro Pro Glu Gln
277         195             200             205
278 Ala Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln
279         210             215             220
280 Asp Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu
281 225             230             235             240
282 Ser Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys
283         245             250             255
284 Ile Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser
285         260             265             270
286 Pro Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala
287         275             280             285
288 Asp Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His
289         290             295             300
290 Ser Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser
291 305             310             315             320
292 Pro Gln Ser Ala Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala
293         325             330             335
294 Ala Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala
295         340             345             350
296 Tyr Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr
297         355             360             365
298 Ser Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala
299         370             375             380
300 Gly Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met
301 385             390             395             400
302 Ser Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro
303         405             410             415
304 Gly Gly Ala Gly Gly Ser Ala Val Asp Asn Pro Leu Pro Asp Tyr Ser
305         420             425             430
306 Leu Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly
307         435             440             445
308 Gly Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala
309         450             455             460
310 Ala His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly
311 465             470             475             480
312 Asp Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Gly
313         485             490             495
314 Tyr Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu
315         500             505             510
316 Ser Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser
317         515             520             525
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319         530             535             540
320 Ala Phe Val Tyr Asp Cys Ser Lys Phe
321 545             550
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VERIFICATION SUMMARY
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